

FIGURE 1

1	ATGTCAGTGGGAGCCATGAAGAGGGAGTGGGGAGGGCAGTTGGGCTTGGAGGGGCGAGC	60
61	GGCTGCCAGGCTACGGAGGAAGACCCCTTCCCGACTCGGGGCTTGGCTCCGGGACAA	120
121	GGTGGCAGGCGCTGGAGGCTGCCGCAGCCTGCGTGGGTGGAGGGGAGCTCAGCTCGGTTG	180
181	TGGGAGCAGGCGACCGGCACCTGGCTGGATGGACCTGGAAGCCTCGTGTGCCACATGGT	240
241	CCCAATGCCAGCAACCTCTGATGGCCCCGATAACCTCACTTCAGCAGGATCACCTCCT	300
301	CGCACGGGAGCATCTCCTACATCAACATCATCATGCCCTTCGGTGTTCGGCACCATCTGC	360
361	CTCCTGGGCATCATCGGGAACCTCCACGGTCATCTTCGCGGTCGTGAAGAGTCCAAGCTG	420
421	CACTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTC	480
481	TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT	540
541	GGGAGACCATGTGCACCCCTCATACGGCCATGGATGCCAATAGTCAGTTCACCAGCACCC	600
601	TACATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC	660
661	ACGAAGTTCCGGAGCCCTCTGTGGCCACCCCTGGTGATCTGCCCTCCTGTGGCCCCCTCTCC	720
721	TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCCTTCCCAGGAGGTGCA	780
781	GTGGCTGCGGCATACGCCCTGCCCAACCCAGACACTGACCTCTACTGGTTACCCCTGTAC	840
841	CAGTTTTCCTGGCCTTTGGCCCTGCCCCCTTGTGTCATCACAGCCGCATACGTGAGGATC	900
901	CTGCAGCGCATGACGTCCCTCAGTGGCCCCCGCCTCCAGCGCAGCATCCGGCTGCGGACA	960
961	AAGAGGTGACCCCGCACAGCCATCGCCATCTGTCTGGTCTTCTTTGTGTGCTGGGCACCC	1020
1021	TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCCTCACCTTTGTCTAC	1080
1081	TTATAAATGCGGCCATCAGCTTGGGCTATGCCAACAAGCTGCCCTCAACCCCTTTGTGTAC	1140
1141	ATCGTGCTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGGTGAAGCCTGCAGCCCCAG	1200
1201	GGCAGCTTCGGCTGTGAGCAACGCTCAGACGGCTGACGAGGAGGAGGACAGAAAGCAA	1260
1261	GGCACCTGA	1269

[illegible]

FIGURE 3

1	M S V G A M K K G V G R A V G L G G G S	20
21	G C Q A T E E D P L P D C G A C A P G Q	40
41	G G R R W R L P Q P A W V E G S S A R L	60
61	W E Q A T G T G W M D L E A S L L P T G	80
81	P N A S N T S D G P D N L T S A G S P P	100
101	R T G S I S Y I N <u>I I M P S V E G T I C</u>	120
121	<u>L L G I I G N S T V I F A V V K K S K L</u>	140
141	H W C N N V P D <u>I F I I N I S V V D L L</u>	160
161	<u>F L L G M P E M I H Q L M G N G V W H F</u>	180
181	G E T M C T L I T A M D <u>A N S O F T S T</u>	200
201	<u>Y I L T A M A I D R Y L A T V H P I S S</u>	220
221	T K F R K P S <u>V A T L V I C L L W A L S</u>	240
241	<u>F I S I T P V W L Y A R L I P F P G G A</u>	260
261	<u>V G C G I R L P N P D T D L Y W F T L Y</u>	280
281	<u>Q E F L A F A L P F V V I T A A Y V R I</u>	300
301	L Q R M T S S V A P A S Q R S I R L R T	320
321	K R V T P T A I A I C L V F F V C W A P	340
341	<u>Y Y V L O L T O L S I S R P T L T F V Y</u>	360
361	<u>L Y N A A I S L G Y A N S C L N P F V Y</u>	380
381	<u>I V L C E T F R K R L V L S V K P A A Q</u>	400
401	G Q L R A V S N A Q T A D E E R T E S K	420
421	G T	422

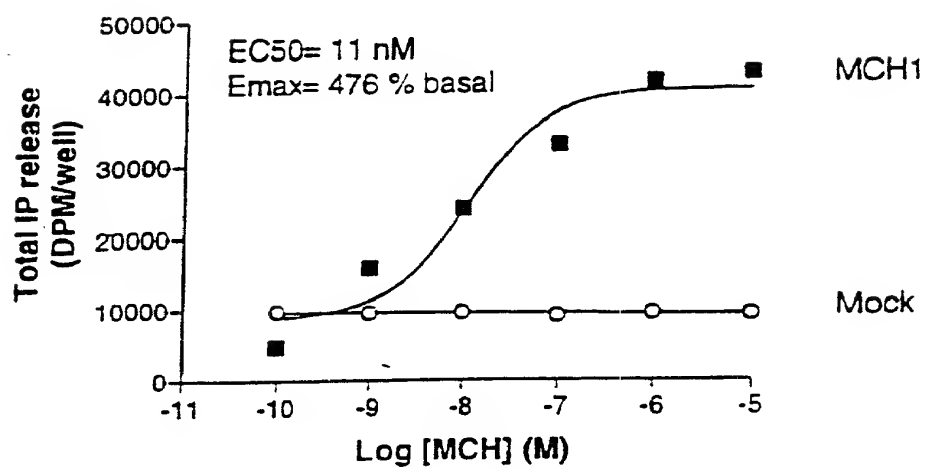
FIGURE 4

1 GCAGGCGACCTGCACCGGCTGCATGGATCTGCAAAACCTCGTTGCTGTCCACTGGCCCCAA 60
 61 TGCCAGCAACATCTCCGATGGCCAGGATAATCTCACATTGCCGGGGTCACTCTCGCAC 120
 121 AGGAGTGTCTCCTACATCAACATCATTTATGCCCTTCCGTGTTGGTACCATCTGTCTCCT 180
 181 GGCATCGTGGGAACTCCACGGTCATCTTTGCTGTGGTGAAGAAGTCCAAGCTACACTG 240
 241 GTGCAGCAACGTCCCCGACATCTTCATCATCAACCTCTCTGTGGTGGATCTGCTTCCT 300
 301 GCTGGGCATGCCCTTTCATGATCCACAGCTCATGGGAACGGCGTCTGGCACTTTGGGGA 360
 361 AACCATGTGCACCTCATCACAGCCATGGACGCCAACAGTCAGTTCACCTAGCACCTACAT 420
 421 CCTGACTGCCATGACCATTTGACCGCTACTTGGCCACCGTCCACCCCATCTCTCCACCAA 480
 481 GTTCCGGAAAGCCCTCCATGGCCACCCCTGGTGATCTGCCCTCCTGTGGGCGCTCTCCTTCAT 540
 541 CAGTATCACCCCTGTGTGGCTCTACGCCAGGCTCATTCCTTCCCAGGGGTGCTGTGGG 600
 601 CTGTGGCATCCGCCCTGCCAAACCCGGACACTGACCTCTACTGTTCACTCTGTACCAGTT 660
 661 TTTCTTGGCCTTTGCCCTTCCGTTTGTGGTCATTACCGCCGCATACGTGAAATACTACA 720
 721 GCGCATGACGTCTTCGGTGGCCCCAGCCCTCCCAACGACAGCATCCGGCTTCGGACAAAGAG 780
 781 GGTGACCCCGCACGGCCATTGCCATCTGTCTGGTCTTCTTGTGTGCTGGCACCCCTACTA 840
 841 TGTGCTGCAGCTGACCCAGCTGTCCATCAGCCGCCCGACCCCTCACGTTTGTCTACTTGA 900
 901 CAACGGGCCATCAGCTTGGGCTATGCTACAGCTGCCTGAACCCCTTTGTGTACATAGT 960
 961 GCTCTGTGAGACCTTTCGAAACCGCTTGGTGTGTGTCAGTGAAGCCTGCAGCCCGGGCA 1020
 1021 GCTCCGCACGGTCAGCAACGCTCAGACAGCTGATGAGGAGAGGACAGAAAGCAAGGCAC 1080
 1081 CTGACAATTCCCCAGTCGCCCTCCAAGTCAGGCCACCCCATCAAACCGTGGGGAGAGATAC 1140
 1141 TGAGATTAAACCCCAAGGCTACCCCTGGGAGAAATGCAGAGGCTGGAGGCTGGGGGCTTGTAG 1200
 1201 CAACCACATTCCAC 1214

1	M	D	L	Q	T	S	L	L	S	T	G	P	N	A	S	N	I	S	G	20
21	Q	D	N	L	T	L	P	G	S	T	P	R	T	G	S	V	Y	D	I	40
41	I	I	M	P	S	V	F	G	S	T	I	L	L	G	S	N	P	S	D	60
61	V	I	F	A	V	V	K	K	S	D	L	H	W	C	S	N	F	F	M	80
81	F	I	I	N	L	S	V	V	G	V	F	F	E	L	T	M	C	I	T	100
101	H	Q	L	M	G	N	S	G	Q	H	L	I	E	T	L	A	M	P	I	120
121	A	M	D	A	N	S	V	F	P	I	A	S	K	F	T	R	K	S	M	140
141	R	Y	L	A	T	C	L	H	L	P	G	L	I	S	I	G	P	V	W	160
161	T	L	V	I	C	L	P	F	P	F	G	L	F	C	I	G	L	P	N	180
181	Y	A	R	T	I	L	D	I	W	F	T	V	Q	F	F	L	A	P	A	200
201	P	D	V	T	V	I	L	T	A	S	I	Q	R	V	M	T	R	S	V	220
221	F	P	V	A	C	I	S	Q	R	F	I	V	K	R	V	T	L	A	I	240
241	P	A	C	I	S	Q	R	F	I	V	C	T	P	F	A	S	I	Q	L	260
261	I	S	I	A	N	S	L	V	R	P	C	S	E	E	R	L	P	G	K	280
281	S	I	A	N	S	L	V	R	P	C	S	E	E	R	L	P	G	K	A	300
301	Y	R	L	T	A	D	E	E	R	L	P	G	K	S	T	P	I	K	L	320
321	R	L	T	A	D	E	E	R	L	P	G	K	S	T	P	I	K	L	H	340
341	Q	T	A	D	E	E	R	L	P	G	K	S	T	P	I	K	L	H	F	354

FIGURE 6

IP release in MCH1- and
mock-transfected Cos-7 cells



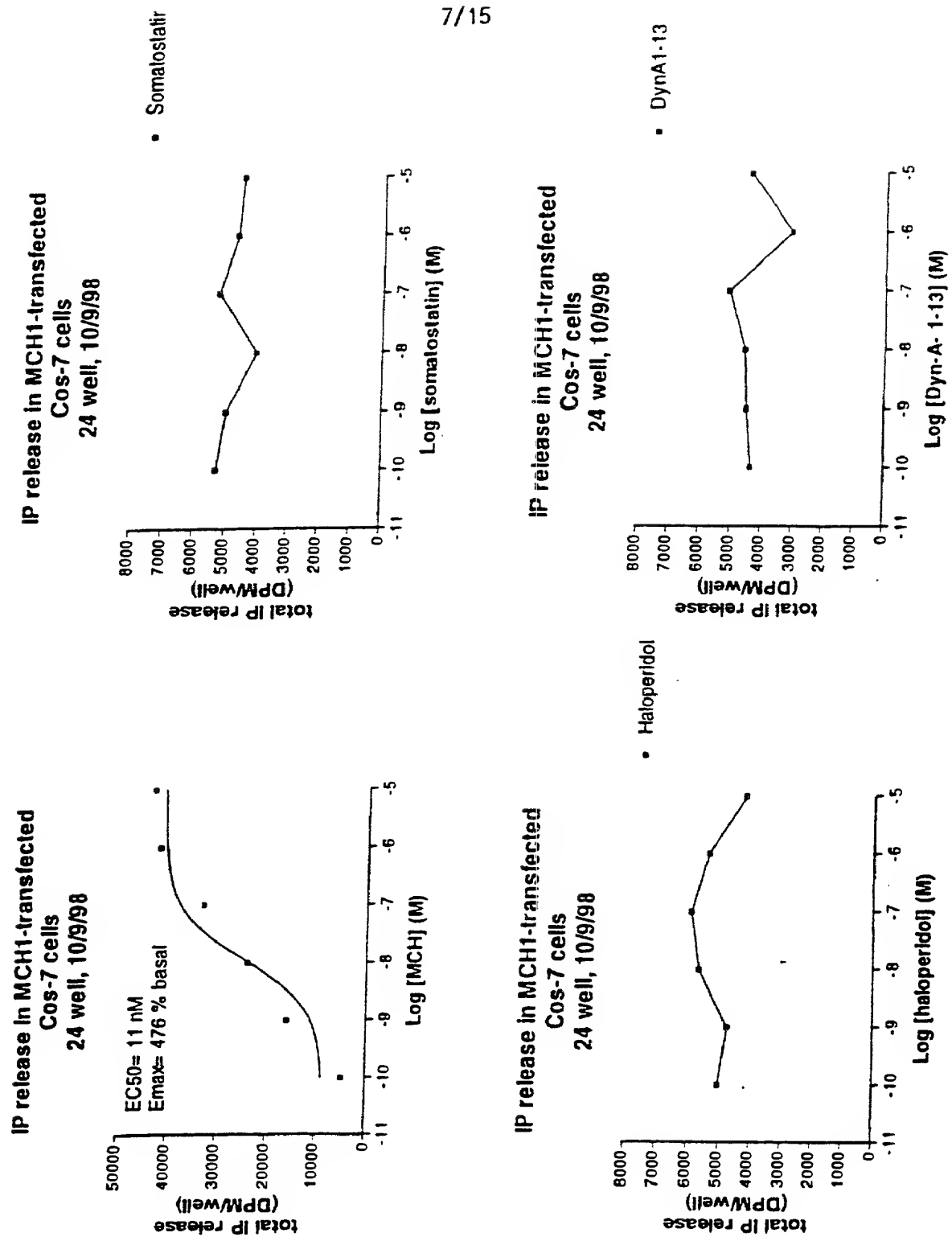


FIGURE 7

Microphysiometer Response CHO cells

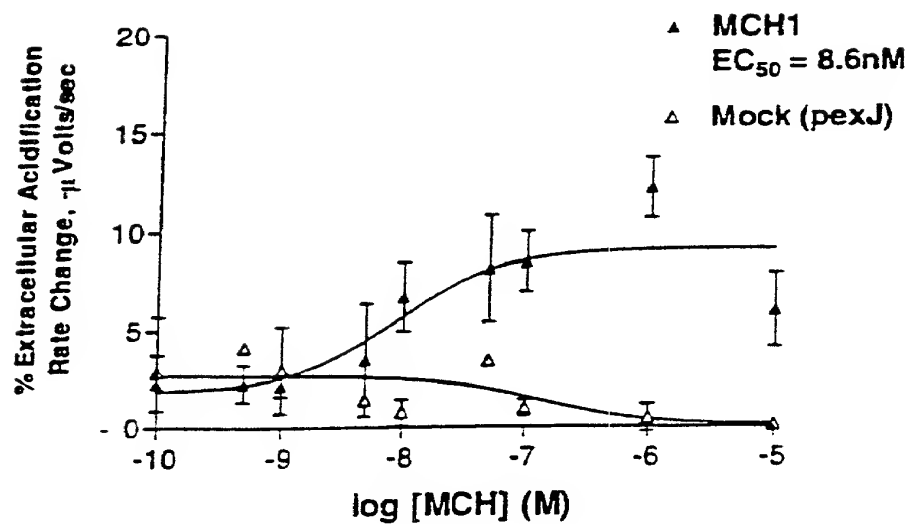
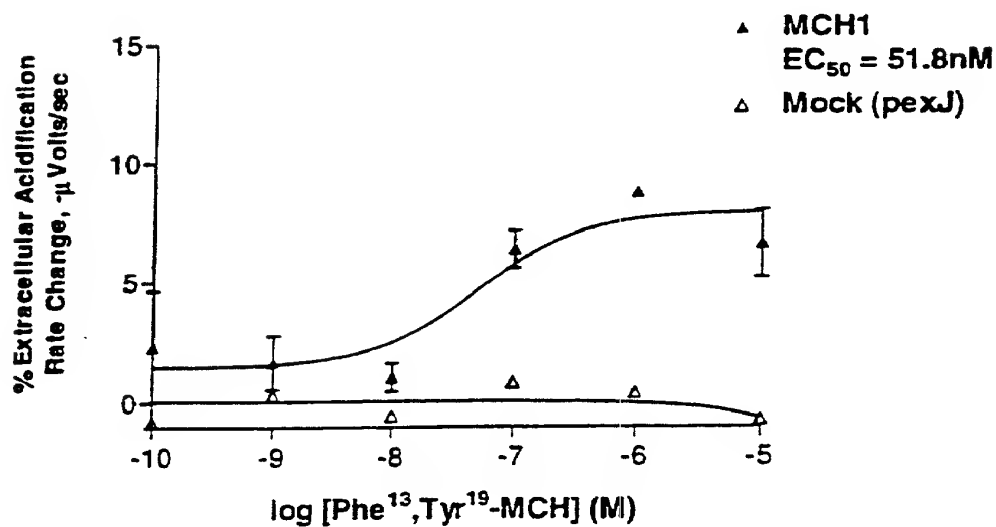


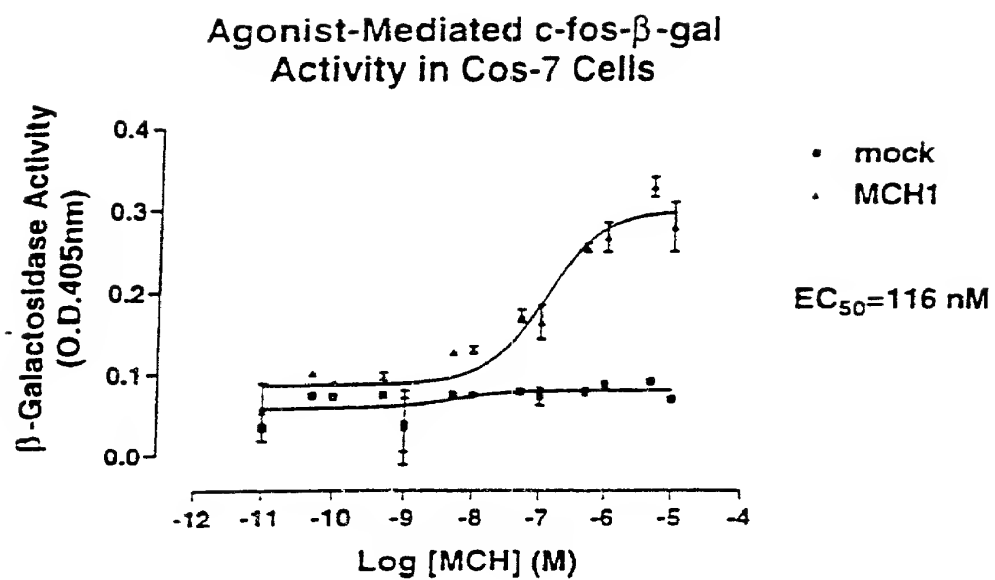
FIGURE 8

Microphysiometer Response CHO cells



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FIGURE 9



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FIGURE 10

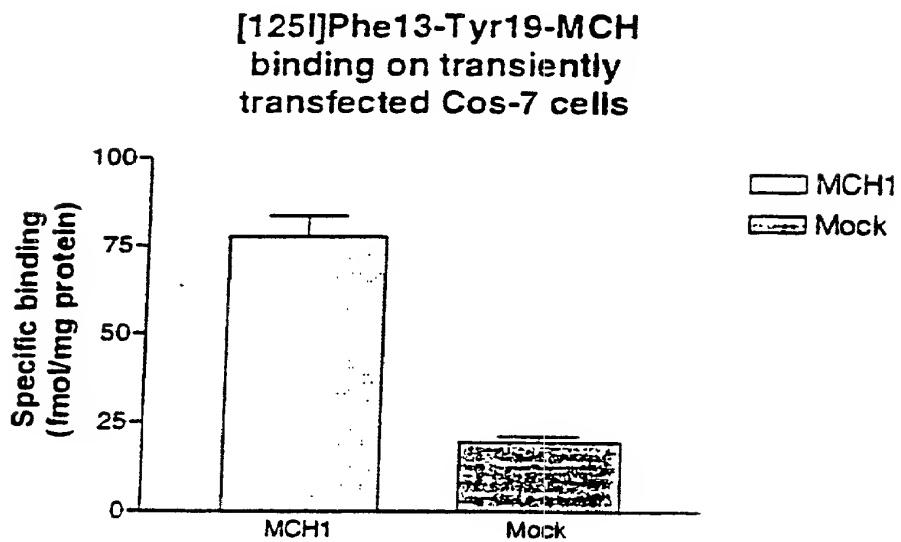
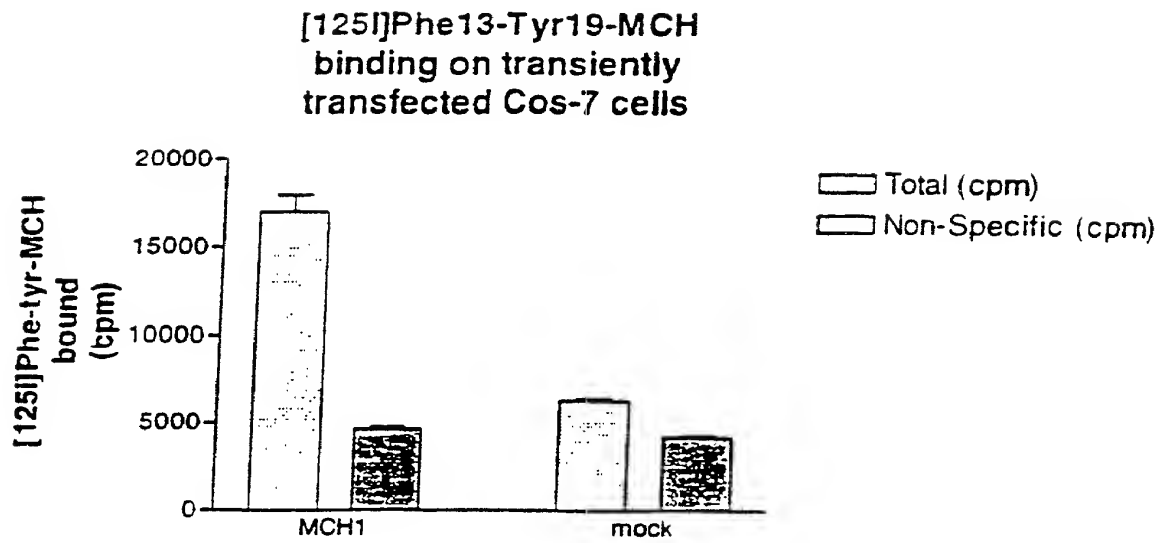
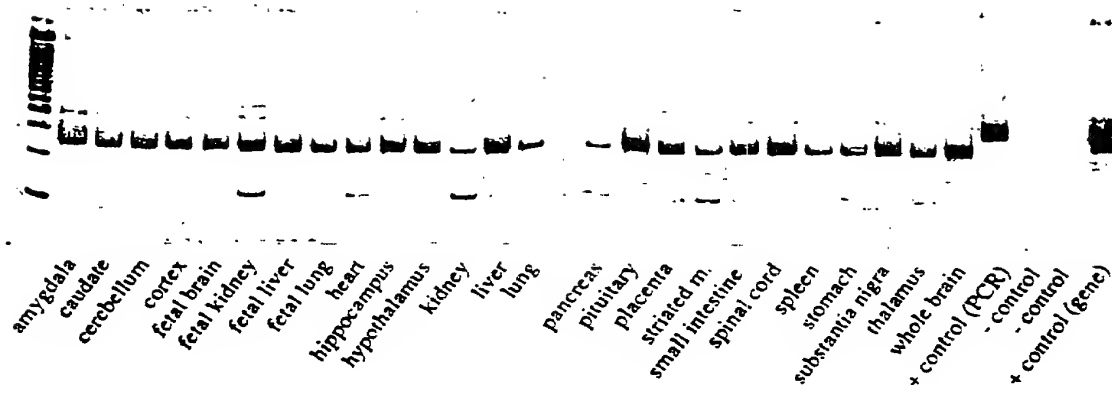


FIGURE 11



[illegible][illegible]

[illegible]

1	M	D	L	E	A	S	L	L	P	T	G	P	N	A	S	N	T	S	D	G	20
21	P	D	N	L	T	S	A	G	S	P	G	R	T	G	S	I	S	Y	I	N	40
41	I	I	M	P	S	V	F	G	T	I	C	L	L	G	I	I	G	N	S	T	60
61	V	I	F	A	V	V	K	K	S	K	L	H	W	C	N	N	V	P	D	I	80
81	F	I	I	N	L	S	V	V	D	L	L	F	L	L	G	M	P	F	M	I	100
101	H	Q	L	M	G	N	G	V	W	H	F	G	E	T	M	C	T	L	I	T	120
121	A	M	D	A	N	S	Q	F	T	S	T	Y	I	L	T	A	M	A	I	D	140
141	R	Y	L	A	T	V	H	P	I	S	S	T	K	F	R	K	P	S	V	A	160
161	T	L	V	I	C	L	L	W	A	L	S	F	I	S	I	T	P	V	W	L	180
181	Y	A	R	L	I	P	F	P	G	G	A	V	G	C	G	I	R	L	P	N	200
201	P	D	T	D	L	Y	W	F	T	L	Y	Q	F	F	L	A	F	A	L	P	220
221	F	V	V	I	T	A	A	Y	V	R	I	L	Q	R	M	T	S	S	V	A	240
241	P	A	S	Q	R	S	I	R	L	R	T	K	R	V	T	R	T	A	I	A	260
261	I	C	L	V	F	F	V	C	W	A	P	Y	Y	V	L	Q	L	T	Q	L	280
281	S	I	S	R	P	T	L	T	F	V	Y	L	Y	N	A	A	I	S	L	G	300
301	Y	A	N	S	C	L	N	P	F	V	Y	I	V	L	C	E	T	F	R	K	320
321	R	L	V	L	S	V	K	P	A	A	Q	G	Q	L	R	A	V	S	N	A	340
341	Q	T	A	D	E	E	R	T	E	S	K	G	T								353